

Fig. 1

HP02573	61'	YGRQDLHLRI	FDPSPEDIARADNI	FTATERNRIDYVSSAVRIDHAPDLPRPEVCFIGRSN
CgpA	1"			MFFAQPVSEFIMGAVRMDAMPSPDLPEVAFAGRSN
HP02573	121'	VGKSSLIKALFSLAPEVEVRVSKKPGHTKKMNF	FKVGKHFVVDM	PGYGF-----RAPED
CgpA	35"	VGKSSLINGL--VNQYLARASNEPGRTRQ	INFFLLAEKVRLVDLP	PGYGFARVSRSLADK
HP02573	176'	FVDMVETYLKERRNLKRTFLLVDSVVG	IQTDNIAIEMCEE	FALPYVIVLTKIDKSSKGH
CgpA	93"	FQDLGRAYLRGRANLKR	VYVLIDARHGLKKVDLEALD	LDVAAVSYQIVLTKADKIKPAE
HP02573	236'	LLKQVLQIQKFVNMKTQ	GCFFQLFPVSAVTFSGIHL	LRCFIASVTGSLD
CgpA	153"	VDKVVAETQKAI	AKRAAA-FPRVLAT	SEKGLGMPELRAEIVRLCIDE

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HP02612 61' KVPLAGGGRKRLHRRHRVYKLVEDTKHRPKENLELILTQSVENVGVRGDLVSVKKSLSGR
      ..***.....* * * * *
      MKLILTADVDHLGSGVGTVEVKDGYGR

RL9_MYCLE 1"

HP02612 121' NRLLPQGLAVYASPENKKLFEEKKLLRQEGKLEKIQTKGAGEALGVVVVAPHTIKLPAEPIT
      * * * * * . * * * . . . . . * * * * *
      NFLIPHGLAIVASRGAQRQADEIRRAR-ETKAMRDREHANEIKVAIEALGVSLSLPMKTVVA

RL9_MYCLE 28" RWGEYWCETVNGLDTVRVPMVSVNFEKPKTKRYKWLAQQAAMAPTSPQI

HP02612 181' DSGKLFSGVTAGDVVAAIKKAGGPNLDKRIVRLPKTHIKAVGTHPVSUHLHPEVDVVVLL
      * . * * * . . . * * . .
      * . * * * . . . * * . .
      * . * * * . . . * * . .

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Fig. 4

HP10120	1'	MQRVGLLSWTLRVLWLSGLSEPGARQPRIMEE-KALEVYDLIRTIRDPKPNTLEEL
CEF45G2		*...*. . . *...*. . . *...*. . . *...*. . . *
HP10120	1"	MGQERLDNANPTLFDKPRHRPVTGTERDESVEPDIDSWEIFDLIRDINDPEHPYTLLEQL
CEF45G2		*...*. . . *...*. . . *...*. . . *...*. . . *
HP10120	60'	EVVSESCVEVQEINEEYLVIIIRFTPTVPHCSLATLIVGNLHF
CEF45G2		*...*. . . *...*. . . *...*. . . *...*. . . *
HP10120	61"	NVQEEELIKV-FIDEEETFVKVNFPTTIPHCSMATLIGLAIRVKLLRLSLHPKVKSVSIT
CEF45G2		*...*. . . *...*. . . *...*. . . *...*. . . *

Fig. 5

HP10421 1' MAAAGLALLCRRVSSALKSSRLTTPQVPACTGFFLSLLPKSTPNVTSEHQYRLLHTTLS
B0261.4 1" MGEAIVRWSALAAHLLFFGSKVFSKIFYFLMFFKSTMWRSLPSLVS-SAVRSQNAVNT
HP10421 61' R--KGLEEFFDDPKNWG----QEKVKSAAWTCQQLRNKSNEDLHKLWYVLLKERNMLLT
B0261.4 58" RFSSTMKQFFDDEANFGKAELRPKHPGRSWTAELRLKSNSDLHKLWYVCLKERNMLIT
HP10421 115' LEQEAQRQLPMPSPERLDKVVDSMDALDKVVQEREDALRLLTGTGQERARPGAWRRDIFG
B0261.4 118" MKKAHTSRARNMPNPERLDRVHETMDRIESVVHERNDVFRLETG-ESAAPRKRTITSA
HP10421 175' RIIWHK-EKQWVIPWHL-NKRYNRKFFALPYVDHFLRLERE---KRARIKARKENLERK
B0261.4 177" GFTYQKQATEHFAPPQLGQKEYETPYLDDDDAYVMQKIQEKEFFMKNRDRLLDDEKRRRAART
HP10421 230' KAKILLKKFFPHLAEAKSSLV
B0261.4 237" EDMDRFKRGAPRVFNR

Fig. 6

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HP10582      1'      MDSNHQSNYKLSKTEKKFLRKQIKAKHTLLRHE-GIETVSYATQSLVVANGGLGN
                * . * . * . * . * . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 361"  RELSYFNEEKAKRIGERFEGGKLAKKVHKHSIEQLKRHDPDVQISTEPTKYLIVSNSSILC

HP10582      55'      GVS RNQLLPV-LEKCGLDALLMPPNKPYPFARYRTTEESKRAYVTLNGKEVVDLGLQKI
                *** . . . * . * . . . * . * . . . * . * . . . * . * . . . * .
YKY5_CAEEL 421"  GVSLEEELEEIFLPLDELAEFIVYPNKRYSFVQCSSIEKSIQVRTELHGLIPPSLKNSHQ

HP10582      114'     TLYLNFVEKVQWKELRPQALPGLMVVEEIISSSEEEKMLLESVDWTEDTDNQNSQKSLKH
                . . . . . * . * . . . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 481"  PFAISYVENLPEATKCEDFRPANLKIIEEYVSSDLEKELVDLV-----TNHPSVQSLKH

HP10582      174'     RRVKHFGYEFHYENNVNVDKDKPLSGGLPDICESFLEKWLKGYIKHKPDQMTINQYEPGQ
                * * * * . * . * . . . * . * . * . . . * . * . * . * . * . * . * .
YKY5_CAEEL 535"  RAVVHFCHVFDYSTNSASEWKE-ADPIPPVINSLIDLRLISDKYITERPDQVTANVYESGH

HP10582      234'     GIPAHIDTHSAFEDEIVSLSLGSEIVMDFKH--PDGIAVPVMLPRRSLVMTGESRYLWT
                *** . * * * * * . * * * . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 594"  GIPSHYDTHSAFDDPIVSI SLSDVVMEFKDGANSARIAPVLLKARSLCLIQGESRYRWK

HP10582      292'     HGITCRKFDTVQASESLKSGIITSDVGDLTLSKRGLRTSFTFRKVRQTPCNCYSYPLVCD
                *** . * * . * . * . * . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 654"  HGIVNRKYD-----V-----DPRTNRVVPVRQTRVSLTLRKIRRKPCCEWKEFCDW

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Fig. 6-1

HP10582 352' QRKETPPSPFESDKESRLQEQYVHQVYEEIAGHFSSTRHTPWP HIVEFLKALPSGSIVA
 .**.. * * * * * . * * * * * . * * * * * . * * * * * . * * * * * . * * * * *
 YKY5_CAEEL 700" DRKGE-MSVPSNEDLALKLENSYVSDVYENIASHFDETRHSSWKAVKQFINEIPRGSVMY
 HP10582 412' DIGCGNGKYLGINKELYMERRVAALQEIVRLLRPGKALLIYVWAMEQEYNKQSKYL RGN
 *.***** * * * * * *
 YKY5_CAEEL 759" DVGCGNGKYL-IPKDGLLKIGCDMCMGLCDIARKKDCHVARCDALALPF-----RYESAD
 HP10582 472' RNSQKGKEEMNSDTSVQSLVEQMRDMGSRDSASSVPRINDSQEGGCNSRQVSN SKLPVH
 * * * * * * * * * * * * * * * *
 YKY5_CAEEL 813" AAISIAVLHHIATFERRKRRLIEELLRVVVKPGSKICVT-VWSMDQSQSEYAKMRGNKDDV-
 HP10582 532' VNRTSFYSQDVLVPWHLKGNPDKG-KPVEPFGPIGSQDPSPVFHRYYHV FREGELEGACR
 * * * * * * * * *
 YKY5_CAEEL 871" AAAPAVSSEETQTTNRLKVHDGKDFEQQDVLVPWTIDQGETFL RYYHV FREGEAEK LIE
 HP10582 591' TVSDVRILQSYVDQGNWC VILQKA
 . * * * * * * . * * * * *
 YKY5_CAEEL 931" SVQGCKKLISVEKEQGNY-III AKKI

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Fig. 8

HP10160	1'	MASRGKTETSKLKQNLQDRLMQQLQDLEECREELDTDEYEETKKETLEQLSEFNDSL
ZK1248	1"	MGVDDLLIKNAQKTIDRLIRQLAEIEQEEENNLEDEYRELREDTVNQLEYGKIV
HP10160	61'	KKIMSGNMTLVDELSGMQLAIQAISQAFTPEVIRLFAKKQPGQLRTRLAEMDRDLMVG
ZK1248	56"	ERLQGGDVSLIDDLTATKIAIRTAISKAFKTPPEIMAFAGKHTGLLREKLMTETNYRSQ
HP10160	121'	KLERDLYTQQKVEILTALRKLGKLTADDEAFLSANAGAILSQFEKVSTDLGSGDKILAL
ZK1248	116"	KMPKQGYLERKFEILMALRRLEETLTEDERKFLSDRLET--PEFQLIEANANRLFSGNVT
HP10160	181'	ASFEVEKTKK
ZK1248	174"	SPVFRVQIMASPKPKKVRLLDDKTENVSPPWKAWWHTKPKRKYTNDKTKESLWDHPNTR

HP10173	1'	MKLLTTHNLLSSHVRGVGSRGFPLRLQATEVTRICPVFENPNFVARMI PKVWSAFLEAADN ***..**.*.*. *.*.*.* .. **..... *.*.*.*.* *
C04H5	1"	MKLFTVHNFMSSRFLKNVTVGYPINLVVKQFVEKDIEFFDRDNTIVMLDRIQYEALIVAAAA
HP10173	61'	LRLIQ-VPKGPFVEGYEE-NEEFLRTMHHLILLEVEVIEGTLCQPESGRMFPISRGI PNMLL * * * * * *
C04H5	61"	VNQSDRIPREKPEKWDELTDQLRVFHHLLMNIDVIDGELICPETKTTFPIRDGIPNMLK
HP10173	119'	SEETEES ..*
C04H5	121"	VDAEK

[illegible]

Fig. 10-1

HP02644 300' DDTVIESEALPSDIAEAEARAKTGTVSDQALLFGDDDDAGEGPSSLIREKFPVKQNEENEENE
CELLF55F8 263" -----
HP02644 360' NLDKEQVGNLQKELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVARFTGIKTA
CELLF55F8 323" -----
HP02644 420' ILVGMSTQKQORML-NRRPEIVVATPGRLWELIKEKHY--HLRNLRLQLRCLVVDEADRM
CELLF55F8 383" SIVGGLAQVKQERIIISQORPDIIVATPGRLWAMMQEAEETGEFLAEWKDLKCLVVDETDRM
HP02644 477' VEKGHFAELSQLEMLNDSQYNPKRQTLVFSATLTLVHQAPARILHKKCHTKGQMDRTAKLD
CELLF55F8 443" VEEGYFAELTHILNKIHEESEKELQTLVFSATLTFKAQDVAEEKCKAKELSSQQKIQ
HP02644 537' LLMQKIGMR-GKPKVIDLTRNEATVETLTETKIH CET-DEKDFYLYCYFLMQYPGRSLVFA
CELLF55F8 503" RLIKLTGLRENKHKVIDLTROMGTAGCLVEARINCGNLLLEKDTSLVYLLTRYPGRTIVFV

Fig. 10-2

[illegible]

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HP03233 1' MAAPGSCALWSYCGRGWGRAMRGCQLLGLRSSWPGDLLSARLLSQEKRAAETHFGFETVS  
      ... * . * * *  
SPUBM 1" MSRLRAPVAKFLADGLKGIRSTALAGURLSN-CRYTSTSSKDDTSSTMTHFGFKDVP  
  
HP03233 61' EEEKGGKVYQVFESVAKKYDVMDNMMSLGIHRVWKDLLWKMHPLPGT--QLLDVAGGT  
      * ** * **.***** *** ***** ..** .....* ..*****  
SPUBM 58" EDEKEHLVKNVFSVAKKYDEMNDAMSLGIHRLWKNI FVSRNLNPNGNSTVPMKILDVAGGT  
  
HP03233 118' GDIAFRFLNYVQSQHQRKKRQLRAQQNL SWEETAKEYQNEDSLGGSRVVVCDINKEML  
      *****.....*..  
SPUBM 118" GDIAFRILNHATNHNGDRNRVIV-----ADINPDMML  
  
HP03233 178' KVG-KQKALAQQYRAG-LAWVLGDAEEL-PFDDDKFDIYTIAFGIRNVTHIDQALQEABR  
      **... ..* * .... ** * . *....***** ** ..***.  
SPUBM 150" SVGLRRSKKTPYYDSGRVEFIEQNAEILDKIPDNSIDMYTIAFGIRNC THIPKVLEQA YR  
  
HP03233 235' VLKPGRFLCLEFSQVNPNLSRLYLDFSVQVIPVLGEVIAGDWKSQYLVESIRRFPSQ  
      ***** * ***** * .. ** *****.****..*****  
SPUBM 210" VLKPPGVFSCLEFSKVYPAPLAELYRQYSFKILPLLGTIIAGDSQSYEYLVESIERFPDA  
  
HP03233 295' EEFKDMI EDAGF---HKVTYESLTSGIVA IHSGFKL  
      ..* ***** ..***. *.***.*..  
SPUBM 270" KTFAKMIEDAGFTLAGETGYETLSFGIAAIHTGIKL
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Fig. 12

1' MQKSCFENEGKPQNMMPKAEEDRPLEDPVQEAEGNPQPSEEGVQEAEGNPRGGPNQPGQG
 ..*.*...*.***.***.***.***.***.
 pp21 1' MKSCQKMEGKPN-----ESEPKEHEEPKPEEKPEEEKLEEEAKAKGTFRERLIQSLQE
 HP10437 61' FKEDTPVRHLDPPEMIRGVDELERLREEIRRVNRNKFVMMHWKQNHRSRYPVCFRP
 ****.***.*.*.*.***. *****.....***.***.
 pp21 56" FKEDIHNRHLSNEDMFREVDEI---DEIRRVNRNKLIVMRWKNRNRNHPYPYLM

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Fig. 14

HP10543	1'	MAATEPILAAATGSPAAVPPEKLEGAGSSSAPERNCVGSLLPEASPPAPEPSSPNAAVPEA
LEAP1	1"	MAAPQSPQDPQSPAAPPEQQEGAGDCA
HP10543	61'	IPTPRAAASAALELPLGPAPVSVAPQAEAEARSTPGPAGSRLGPETFRQFRQFRYQDAA
LEAP1	28"	APSPDSGSSPAPELPGAPAAALNTAPYADAVLR---PGASRPGPETFRQFRQFRYQDAA
HP10543	121'	GPREAFRQLRELSRQWLRPDIRTKEQIVEMLVQEQLLAILPEAARARRIRRTDVRITG
LEAP1	84"	GPREAFRQLRELSRQWLRPDIRTKEQIVEMLVQEQQLAILPEAARARRIRRRADVIRITG

Fig. 15

HP03090 1' MAARRALHFVKVGNRFQTARFYRDVLGMKVLRHEEFEEGCKAACNGPYDGKWSKTMVGF
 CEHYPO 1" M'ARALHYVFKVANRAKTIDFFTNVLNMKVLRHEEFEEGCKEATCNGPYNGRWSKTMIGY
 HP03090 61' GPEDDHFVAELTYNYGVGDYKLGNDFMGITLASSQAVSNARKLEWPLTEVAEGVFETEAP
 CEHYPO 60" GSEDEHFVLEITYNYPIHKVELGNDYRAIVIDSDQLFEKVEKIN--HRKSGCGRLAVKDP
 HP03090 121' GGYKFYLNQNRSLPQSDPVLKVTLAVSDLQKSLNYWCNLLGMKIYEKDEEKQALLGYADN
 CEHYPO 118" DGHEF--KIGKADQSPKVLRVQNVNVDLEKSKKYWNETLGMPIVEEEKSSRIR--MSYGDG
 HP03090 181' QCKLELQGVKGGVDHAAAFGRIAFSCPQKELPDLEDLMKRENQKILTPLVSLDTPGKATV
 CEHYPO 174" QCELEIVKSQDKIDRKTFGRIAFSYPEDKLESQDKIKSANGTIINELTTLETTPGKADV
 HP03090 241' QVVILADPDGHEICFVGDEAFRELSKMDPEGSKLLDDAMAADKSDEWFAKHNKPKASG
 CEHYPO 234" QVVILADPDEHEICFVGDEGFRALSKIDDKAESLKEQIKKDDSEKWI

Fig. 16

HP03145 1' MLGSRAGFARGLRALAWLPGWGRGRSFALARAAGAPHGGDLQPPACPEPRGRQLSLSA
 SCCOQ2 1" MIIKPIASPARYFLRTPSWSAVAIFQAVKIKPLQLRNTSSNSVTPNLISPSK
 HP03145 61' AAVVDSAPRPLQPYLRIMRLDKPIGTWLLYLPCWISIGLAA---EPGCFPDWYMLSLFGT
 SCCOQ2 53" KSWKDLFSKRWQYVAEISRAGSPTGTLYLLYSPCTWISILMAAYAYDSSLVNVTKMLALEGV
 HP03145 118' GAILMRGAGCTINDMWDQDYDKVTRTANRPIAAGDISTFQSFVFLGGQLTLALGVLLCL
 SCCOQ2 113" GSFLMRGAGCVINDLWDRELDKAKVERSKSRPLASGKLSVRQAISSLVQLTASLGILLQL
 HP03145 178' NYYSIALGAGSLLLVITYPLMKRISYWPQALGLTFNMGALLGWSA IKG-SC-DPSVCLP
 SCCOQ2 173" NPYTIKLGVASLVPCITYPAMKRITYYPQVVLGLTFGYGAVMGWPALAGEACMNWSVVAP
 HP03145 236' LYFSGVMWTLIYDIYAHQDKRDDVLLIGLKSTALRFGENTKFWLPGFVAMLGALSLVGV
 SCCOQ2 233" LYLSTISWIVLYDIYAHQDKRDDVVKANIYSTALRFGDNTKFWLPGFVAMLGALSLVGV
 HP03145 296' NSGQTAPYYA-ALGAVGAHLTHQIYTLDIHRPDCWNKFISNRTGLIVFLGIVLGNLWK
 SCCOQ2 293" MNGQGPVFTYTLGVAGAAVRLSSMIYKVDLDDPKDCFRWFKRNSNTGYLVAAAIALDWLAK
 HP03145 355' EKKTDKTKKGIENKIEN
 SCCOQ2 353" SFIYDS

Fig. 17

[illegible]

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Fig. 18

HP03324	1'	MALCALTRALRSLNLPPTVAAPAPSLFPAAQMMNNGLLQQPSALMLLPCRPLTTSVALN	
BRPL2	1"		MGLKRFPVTPGRRFMVI
HP03324	61'	ANFVSWKSRTKYTITPVMRKSGGRDHTGRIRVHVGIGGGHKQRYRMIDFLRPERPEETKSG	
BRPL2	19"	SDFS DITKTEPEKSL LAPLKKTGGRNHHGRVTVRHRRGGGKKRRYRIIDFKRY-----DKAG	
HP03324	121'	PFEKVIQVRYPDCRSADIALVA-GGSRKRWIIATENMQAGDTILNSNHIGRWAVAAREG	
BRPL2	75"	-IPAKVLAIEYDPNRSARIALLLYADGEKRYILAPKGVNVGDTILMSGPD---AEIRP---G	
HP03324	180'	DAHPLGALPVGTLINNVESEPGRGAQYIRAAGAGNVRNSRPSIQR	
BRPL2	129"	NALPLEKIPVGTLVHNVEFTPGKGGQIARAAGTYCQIMAKEGNYALLRMPGSELKRVHIK	

Fig. 20

HP10162	1'	MEPQEERETQVAAWLKKIFGDHPPIQYEVNPRTEILHHLSENRVRDRDVYLVIEDLKQ
RNUNK	1"	MAALEEKASQVAEWLKKIFGDHPPIQYEMNARTTEILYHLSERNVRDRDVNLVIEDLRP
HP10162	61'	KASEYESEAKYLQDLLMESVNFSPANLSSTGSRYLNALVDSVAVALETKDTSASFIPAVN
RNUNK	61"	KASEYESEAKRLIEDFLMESVNFSPANLSNTGSRFLNALVDSIAIALEIKDTSASFIPAVN
HP10162	121'	DLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDVKKAEHLSTERAKVDNRRQ
RNUNK	121"	DLTSDLFRTKSKSEEIKLEIGKLEKNLTATLVLEKCLREDLKKADVHLAERAKAEGRLQ
HP10162	181'	NMDFLKAKSEEFRRFGIKAAEEQLSARGMDASLSHQSLVALSEKLARLKQQTIPLKKKLES
RNUNK	181"	NMDFLKAKAAEFRRFGIRAAEEQLSSRGMDASLSHRSLVALSDKLSELKQQTIPLKKKLES
HP10162	241'	YLDLMPNPSLAQVKIEEAKRELDLSIEAELTRRVDMMEL
RNUNK	241"	YLDLMPNPSLAQVKIEEAKRELDIAIEAELTKKVDMMEL

Fig. 21

HP10334 1' MSGLRVYSTVSGSREIKSQSQSEVTRILDGKRIQYQLVDISQDNALRDEM---ALAGNP
 HSSH3 1" MVIRVYIASSSGSTAIAKKKQDVLGFLANKIGFEEKDIAANEENRKWMRENVPENSRP
 HP10334 58' KAT---PPQIVNGDQYCGDYELFVEAQNTLQEFKLKLA
 HSSH3 60" ATGYPLPPQIFNESQYRGDYDAFFARENNNAVYAFGLTAPPGSKEAEVQAKQQA

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Fig. 22

HP10532	1'	MAGSEELGLREDTLRVLAFLRRGEAAGSPVPTPPRSPAQEEPTDFLSRLRRCLPCSLGR
HSBBK	1"	MAGSEELGLREDTLRVLAFLRRGEAAGSPVPTPP-SPAQEEPTDFLSRLRRCLPCSLGR
HP10532	61'	GAAPSESPPRCSLPIRPCYGLEPGPATPDFYALVAQRLEQLVQEQLKSPSPPELQGPST
HSBBK	60"	GAAPSESPPRCSLPIRPCYGLEPGPATPDFYALVAQRLEQLVQEQLKSPSPPELQGPST
HP10532	121'	EKEAILRRLVALLLEEEAEVINQK-----
HSBBK	120"	EKEAILRRLVALLLEEEAEVINQKLASDPALRSKLVRLSSDSFARLVELFCSRDDSSRPSR
HP10532	181'	-----EGILAV
HSBBK	180"	ACPGPPPPSPEPLARLALAMELSRRVAGLGGLAGLSVEHVHSFTTPWIQAHHGWEGILAV
HP10532	241'	SPVDLNLPLD
HSBBK	240"	SPVDLNLPLD

F i g. 2 4

HP10562 61' QESEPEDFKLFDIDNEVVCSEASPGSDSGISEDPCHPDPPAPRATSSPMLYEVVYEAG
LZIP 1" MELELDAGDQDILLAFLEESGDLGTAPDEAVRAPLDWALPLSEVPDWEVDDDL
HP10562 121' ALERMQGETGPNVGLISIQDQWSPAFMVPDSCMVSELPFDAHAILPRAGTVAPVPCIT
LZIP 54" LCSSLSPPASNLILSSSNPCLVHHDHTYSLPRETVSMDLESESCRKEGTQMTPOHMEELA
HP10562 181' LLPQCFTLTDEEKRLGQEGVSLPShLPLTKAEERVLKKVRRKIRNKQSAQDSRRRKKKE
LZIP 114" EQETARLVLTDEEKSLLLEKEGLILPETPLTKTEEQILKRVRRKIRNKRSQAQESRRKKKV
HP10562 241' YIDGLESRVAAACSAQNQELQKKVQELERHNI SLVAQLRQLQTLIAQTSNKAAQTSTCVLI
LZIP 174" YVGGLESRVLKQYTAQNMELOQNVQVQLLEEQNL SLDDQLRKLQAMVIEISNKTSSSSTCILV
HP10562 301' LLFSLALIILPSFSPFQSR----PEAGSEDYQPHGVTSRN--ILTHKDV TENLETQVVES
LZIP 234" LLVSFCLLVVPAMYSSDTRGSLPAEHGVL SRQLRALPSEDPPYQLELPALQSEVPKDS THQ
HP10562 355' RLREPPGAKDANGSTRTLLEKMGKPRPSGRIRSVLHADEM
LZIP 294" WLDGSDCVLQAPGNTSCLLHYMPQAPSAEPPLEWFFDLFSEPLCRGPILPLQANLTRKG

Fig. 25

HP10456	1'	MSNMEKHLFNLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAEN *****
CEBC-2	1"	MGAGESSSMALEKHLFDLKFAAKQLEKNAQRCEKDEKVEKDKLTAAIKKGNKEVAQVHAEN *****
HP10456	55'	AIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVKSMDATLKTNNLEKISAL *****
CEBC-2	61"	AIRKKNQAVNYIKMAARIDAVAAARVQTAATQKRVTASMSGVVKAMESAMKSMNLEKVQQL *****
HP10456	115'	MDKFEHQFETLDVQTTQMEDTMSSTTTLTTPQNQVDMLLOEMADEAGLDLNMELPQGQTG *****
CEBC-2	121"	MDRFERDFEDLDVTTKTMEKTMGTGVINAPKQSQVDALIAEAADKAGIELNQELPSNVPT *****
HP10456	175'	SVGTSV-ASAEQDELSQRLARLDQV .. * .. * .. * .. *
CEBC-2	181"	ALPTGTQAVSEDKDLTERLAALRNM

Fig. 26

HP10498	1'	MATPSLRGLARFGNPRKPVLPKNKPLILANRV-GERRREKGEATCITEMSVMA
CEC24	1"	MMFSSPLLKEKALARGKSIYPKVAVFSEILPLASKNRVQAGQKPRAASSSCTQELQALFG
HP10498	55'	CWKQNEFRDDACRKEIQGFIDCAAR-AQEARKMR--SIQETLGESGSLLPNKNLKLQRF
CEC24	61"	CLKKWEFDDVPCSKQHTLYMDCVHKGAEEAAAYRDATRKGTLGESGAGGKQSMTSAQFNK
HP10498	112'	PNKP YLS
CEC24	121"	IQKLFPQPDLGKQPYRQMKRLPTQDYADDTFHRKHWSGKRS

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Fig. 27

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HP10505 1' MAKHLKFIARTVMVQEGNVESAYRTLNRILITMDGLIEDIKHRRYYEKPCCRRRQRRESYERC
          ***...*. *... *... *... *... *... *... *... *... *... *... *... *... *...
CEF29   1" MVQNNNDVDGAFGLNRLNLDSEGMLKIIRRTQFYQPYMQRKRTLSEAS
          ***...*. *... *... *... *... *... *... *... *... *... *... *... *... *...
HP10505 61' RRIYNMEMARKINFLMRKNRADPWQC
          **..*****.*...*...
CEF29   49" TAIFNEDMNRKMCKFLVRKNRPDKHPGGVTS

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HP10515 1' MFLTAL-LWRGRIPGRQWIGKHRRPRFVSLRAKQNMRRLREIEAENHYWLSPYMTREQE
          * * . * . * . * . * . * . * . * . * . * . * . * . * . * . * .
DM63B   1" MHLTLINLFKKTVPGHIFRGKRRLVKPVSRAMDTLTREYERQEQVMLLLRHPYLTMEEQS

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Fig. 29

HP01124	1'	MGTEKESPEPDCQKQFQAAVSVIQNLPKNGSYRPSYEEMLRFYKYKQATMGPCLVPRPG
HSACBP	1'	MSQAEEFEKAAEEVRHL-----KTKPSDEEMLFYGHYKQATVGDINTERPG
HP01124	60'	FWDPIGRYKWDWNLSLGKMSREEMSAYITEMKLVAKVIDTVPLGEVAEDMFGYFEPLY
HSACBP	47"	MLDFTGKAKWDWNELKGTSKEDAMKAYINKVEELKKYGI


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HP10101 1' MKAVKSEREGSRRRHRDGDVVLPAQVVVKQERLSPEVAPPAAHRRPDHSGGSPFPPTSEP
HP10101 60' ARSGHRGNRARGVSRSPPKKKNKASGRRSKSPRSKRNRSPHHSTVKVKQEREDHPRRGRE
CEC32E8 1' MGRDSPRDRRRHRDRSPERRRRSRSRDRQTRRD-T
HP10101 121' DRQHREPSEQEHRRRARNSDRRHRGHSHQRRTSNERPGSQGQGRDRDTQNLQAQEEERE
CEC32E8 36" RRDDSPKIKREVKEEQFSDNDSPPRRRDDRGRRDRDRDRNRDDR-RDHRDDRGDRDRDRD
HP10101 181' FYNARRREHRQNDVGGGSESQELVPRPGNNKEKEVPAKEKPSFELSGALLIEDTNTFR
CEC32E8 95" NF--RRDPVREDGKQYGLEKKEENWGKPEEPAKEK-----EKVNLGTSGALLIEDTNTFR
HP10101 241' GVVIKYSEPPEARIPKKRWRLYPFKNDEVLPVMIYIHRQSAVLLGRHRRRIADIPIDHPSCS
CEC32E8 148" GVVIKYNPEPEAKPNARWRLYPFKGGEESQVLYIHRQSAVLLIGRDHKIADIPVDHPSCS
HP10101 301' KQHAVFQYRLVETRADGTVGRRVKPYIIDLGSGNGTFLNNKRIEQRYRYELKEKDVLKF
CEC32E8 208" KQHAVLQFRSMFPFTRDDGTKARRIMPYIIDLGSGNGTFLNEKKIEPQRYIELQEKDMLKF
HP10101 361' GFSSREYVLLHESDTSIEDRKDDDEDEEEEEEVSIDS
CEC32E8 268" GFSTREYVVMKEREITEEELAEGEDVVKKEESD

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HP10101 361' GFSSREYVLLHESSTSEIDRKDDDEFEFEFEVSDS
 ..***.***.***.***.***.***.
 CEC32E8 268" GFSTREYVVMKEREITEEELAEGEDVKKKEESD

Fig. 32

HP10370 1' MEYDEKLARFRQAHLNPFNKQSGPRQHEQQPGFEVDPVTPKALPELPPQEPEF
 DMCg115 1" MSSWKDSLTSGTVAQLINESASNLLHSSSTLGSTVGLGGSGTSGGSEAGGSEESGPQ
 HP10370 55' RCPERVMDLGLBEDHFBRPVGFLFIASDVQQLRQAIEECKQVILELPEQSEKQKDAVVRLI
 DMCg115 61" GAERYALPFPASIVREQWRLITFSDANIQDLQAATAHCNDLVLSEELSEERRWLVRHLV
 HP10370 115' HLRKLQELKDPNE-----DEPNIRVLEHNE-----YKEKSKSVKQTCDK
 DMCg115 121" DLRYSLQELEEAQEQHSLSSDMVMNAIRAVVGHIFVPIPHIHGKRRRLQAAAKRNYCDH
 HP10370 156' CNTTIWGLIQTWYTCGYYRCHSKCINLISKPCVSSKVS HQAEYELNICPETGLDSQDY
 DMCg115 181" CTTIISVVQNSVVCSDCGFLVHQKCIDGVKRVCAINVLVSEHQHPISIEICPEIGLASQGY
 HP10370 216' RCAECRAPISLRGVSEARQCDYTGQYYCSHCINWDLAVIPARVVHWNWDEFPRKVSRCSM
 DMCg115 241" KCAECGTMLNKNITWIEPNLCDYSGLYCPCRCNWNDSNFIPARIINWDFHPRRVSR TAL
 HP10370 276' RYLAIMVSRPVLRIREINPLILFYSVVEELVEIRKLQDILLMKPYFITCREAMKARLL-LQ
 DMCg115 301" QEIRLFLNKPILIRLEEDNPKLFVFEKLCVAVKKLRQNLVIMRHVYLAACKIASSELKLVDDQ
 HP10370 335' LQDRQHFTVENDEMYSVQDLLDVHAGRLGCSLTETHTLFAKHKLDCERCQAKGFVCELCH
 DMCg115 361" LGVRRHLAQSNFEFYBLSDLSQVESGALJEFLOGVFKAFNDHIR-SCPMCLAQAYICEICS
 HP10370 395' EGDVLFPPFDSHT"SVACDCSAVTHRDCYTDNSTTCPCKCARLSLRKQSLFQEPGPDVEA
 DMCg115 420" NNEVIFPFDGCIKCDQCNSIFHRVCLTRKNMICPKCIRIQERRRLQDRMKSTEDDDDDDD

Fig. 33

HP10427 1' MAGPAAAFRRRLGALSGAAALGFASYGAH---GAQFPDAYGKELFDKANKHHFLHSLALLG
 ... ***** * * * * *
 CEY106G 1" MSPIIRLAGLSGAVAISLGAYGSHVLRDNP SIDERRRTAFDTASRYHLIHSALALA
 HP10427 58' VPHCRKPLWAGLLLASGTTLECTSFYYQALSGDPSIQTLAPAGGTLILLGLWALAL
 * * * * * * * * * *
 CEY106G 57" SPAARFPLVTAGLFTAGITLFCGPCYHYSISGVETTRKYTPPIGGVTLLIIAWLSFIL

Fig. 34

HP10516 1' MAGTGLIALRTLPGPSWVRGSPVLSRLQDAAVVRPGFLSTAEETLSRELEPEIRRRR
 DMC141 1" MRIITDFISEPEEQQLHEEIEPYMSRLR
 HP10516 61' YEYDHWDAATHGPRETEKSRWSEASRAILQRVQAAAFPGQTLLSSVHVLDLEARGYIKP
 DMC141 29" YEFDHWDDAITHGPRETERKKWFPKNREILERVQRQVAF--DGAVMPYVHILDLPDGVIKP
 HP10516 121' HVDSIKFCGATIAGLSLSPVMRLVHT-----QEPG
 DMC141 87" HVDSTRYCGNTISGISLSDSVMRLVRTDEQRYQQQSSGTATDPNSQGSPEPDAAVYRHQPE
 HP10516 153' EWL-----ELLEPGSLYILRGSAARYDFSHEILRDEESFFGERRIPRGRRISVICRSLP
 DMC141 147" ASLKNFYADILLPRRSLYIMSHYARYKFTHEILAKEHSQFGALVPRTRRISICRNEP

Fig. 35

HP10580 1' MKKFFQEFKADIKFK
DMCG546 61" TLLKVLIVLLGTCVLGYSWSIYGVKVI TEKFVRPSTLKEIEELKLSKAEAAFKLNL TGS
HP10580 16' SAGPGQKLKESVGEKAHKEPNQ--PAPRPPRQGP TNEAQMAAAALARLEKQKQSRWGP
DMCG546 121" GMGTGHLNSPKQETPSSSRQKYEA YVPPKRNEISNEARAAAALARIDKRTSREFN-
HP10580 74' TSQDTIRNQVRKELQAEATVSGSP-EAPGTNVVSEPREEGSA-HLAVPGVYFTCPL-TGA
DMCG546 180" TSLSAVKAQAKRELEAEERRQREEMGTPSTSTSTASGGDTRNLACEGVFFRCPLISEE
HP10580 131' TLRKQDQDACEIKAEAILLHFSTDPVAASIMKIYTFNKDQDRVKLGVD TIAKYLDNIHLHPE
DMCG546 240" ILPKSVWKVRIKEFLYQQLEADRGLTACLI IHNCN-VKEKADECIATLIRYLENL IKNPE
HP10580 191' EEKYRKIKLQNKVFQERINCLGTHEFFEAIGFQKVLLPAQDQEDPEEFYVLS ETTLAQP
DMCG546 299" EEKFKIRMSNKIFSEKVRVVEGALDVLQAAGFNEV-----QIDGEPFL LWTKEQTEKD

Fig. 35-1

[illegible]